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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/992,524

DATE: 01/26/2002  
 TIME: 14:04:41

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1 <110> APPLICANT: Vasquez, Maximiliano  
 2 Landolfi, Nicholas F.  
 3 Tsurushita, Naoya  
 4 Queen, Cary L.  
 5 Protein Design Labs, Inc.  
 6 <120> TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon  
 7 <130> FILE REFERENCE: 011823-008110US  
 8 <140> CURRENT APPLICATION NUMBER: US/09/992,524  
 9 <141> CURRENT FILING DATE: 2001-11-13  
 10 <150> PRIOR APPLICATION NUMBER: 09/450,520  
 11 <151> PRIOR FILING DATE: 1999-11-29  
 12 <160> NUMBER OF SEQ ID NOS: 13  
 13 <170> SOFTWARE: PatentIn Ver. 2.1  
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 21 <222> LOCATION: (1)..(381)  
 22 <223> OTHER INFORMATION: AF2 VL  
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 1 5 10 15  
 ggt gct gat ggg aac att gtt atg acc caa tct ccc aaa tcc atg tac 96  
 Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Tyr  
 20 25 30  
 gtg tca ata gga gag agg gtc acc ttg agc tgc aag gcc agt gaa aat 144  
 Val Ser Ile Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn  
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 Val Asp Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro  
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 Lys Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp  
 65 70 75 80  
 cgc ttc acg ggc agt gga tct gca aca gat ttc act ctg acc atc agc 288  
 Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser  
 85 90 95  
 agt gtg cag gct gaa gac ctt gca gat tat cac tgt gga cag agt tac 336  
 Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Ser Tyr  
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45      aac tat cca ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aag      381
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59          20            25            30
60      Val Ser Ile Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn
61          35            40            45
62      Val Asp Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro
63          50            55            60
64      Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp
65          65            70            75            80
66      Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser
67          85            90            95
68      Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Ser Tyr
69          100           105           110
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79 <222> LOCATION: (1)..(408)
80 <223> OTHER INFORMATION: Description of Artificial Sequence:AF2 VH
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83      Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
84          1             5             10            15
85      gtc ctc tcc cag gtc caa ctg cag cag cct ggg gct gac ctt gtg atg      96
86      Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Asp Leu Val Met
87          20            25            30
88      cct ggg gct cca gtg aag ctg tcc tgc ttg gct tct ggc tac atc ttc      144
89      Pro Gly Ala Pro Val Lys Leu Ser Cys Leu Ala Ser Gly Tyr Ile Phe
90          35            40            45
91      acc agc tcc tgg ata aac tgg gtg aag cag agg cct gga cga ggc ctc      192
92      Thr Ser Ser Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Arg Gly Leu
93          50            55            60
94      gag tgg att gga agg att gat cct tcc gat ggt gaa gtt cac tac aat      240
95      Glu Trp Ile Gly Arg Ile Asp Pro Ser Asp Gly Glu Val His Tyr Asn

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98	Gln Asp Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser			
99	85	90	95	
100	aca gcc tac atc caa ctc aac agc ctg aca tct gag gac tct gcg gtc			336
101	Thr Ala Tyr Ile Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val			
102	100	105	110	
103	tat tac tgt gct aga gga ttt ctg ccc tgg ttt gct gac tgg ggc caa			384
104	Tyr Tyr Cys Ala Arg Gly Phe Leu Pro Trp Phe Ala Asp Trp Gly Gln			
105	115	120	125	
106	ggg act ctg gtc act gtc tct gca			408
107	Gly Thr Leu Val Thr Val Ser Ala			
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120	20	25	30	
121	Pro Gly Ala Pro Val Lys Leu Ser Cys Leu Ala Ser Gly Tyr Ile Phe			
122	35	40	45	
123	Thr Ser Ser Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Arg Gly Leu			
124	50	55	60	
125	Glu Trp Ile Gly Arg Ile Asp Pro Ser Asp Gly Glu Val His Tyr Asn			
126	65	70	75	80
127	Gln Asp Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser			
128	85	90	95	
129	Thr Ala Tyr Ile Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val			
130	100	105	110	
131	Tyr Tyr Cys Ala Arg Gly Phe Leu Pro Trp Phe Ala Asp Trp Gly Gln			
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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/992,524

DATE: 01/26/2002  
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147 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
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149 gga tca acc gga gat att cag atg acc cag tct ccg tcg acc ctc tct 96
150 Gly Ser Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
151 20 25 30
152 gct agc gtc ggg gat agg gtc acc ata acc tgc aag gcc agt gaa aat 144
153 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asn
154 35 40 45
155 gtg gat act tat gta tcc tgg tat cag cag aag cca ggc aaa gct ccc 192
156 Val Asp Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
157 50 55 60
158 aag ctt cta att tat ggg gca tcc aac cgg tac act ggg gta cct tca 240
159 Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser
160 65 70 75 80
161 cgc ttc agt ggc agt gga tct ggg acc gat ttc acc ctc aca atc agc 288
162 Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
163 85 90 95
164 tct ctg cag cca gat gat ttc gcc act tat tac tgc gga cag agt tac 336
165 Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Ser Tyr
166 100 105 110
167 aac tat cca ttc acg ttc ggt cag ggg acc aag gtg gag gtc aaa cgt 384
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172 <211> LENGTH: 128
173 <212> TYPE: PRT
174 <213> ORGANISM: Artificial Sequence
175 <220> FEATURE:
176 <223> OTHER INFORMATION: Description of Artificial Sequence:human-mouse
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181 Gly Ser Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
182 20 25 30
183 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asn
184 35 40 45
185 Val Asp Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
186 50 55 60
187 Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser
188 65 70 75 80
189 Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
190 85 90 95
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194 115 120 125
196 <210> SEQ ID NO: 7
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 203 <221> NAME/KEY: CDS  
 204 <222> LOCATION: (1)..(408)  
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 1 5 10 15  
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 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Leu Lys Lys  
 20 25 30  
 cct ggg agc tcc gtg aag gtc tcc tgc aaa gct tct ggc tac atc ttt 144  
 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe  
 35 40 45  
 act agc tcc tgg ata aac tgg gta aag cag gcc cct gga cag ggt ctc 192  
 Thr Ser Ser Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu  
 50 55 60  
 gag tgg att gga agg att gat cct tcc gat ggt gaa gtt cac tac aat 240  
 Glu Trp Ile Gly Arg Ile Asp Pro Ser Asp Gly Glu Val His Tyr Asn  
 65 70 75 80  
 caa gat ttc aag gac aag gct aca ctt aca gtc gac aaa tcc acc aat 288  
 Gln Asp Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Asn  
 85 90 95  
 aca gcc tac atg gaa ctg agc agc ctg aga tca gag gac act gca gtc 336  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110  
 tat tac tgt gca aga gga ttt ctg ccc tgg ttt gct gac tgg ggc caa 384  
 Tyr Tyr Cys Ala Arg Gly Phe Leu Pro Trp Phe Ala Asp Trp Gly Gln  
 115 120 125  
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 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe  
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VERIFICATION SUMMARY  
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